

SEQUENCE LISTING

<110> Director-General of Agency of Industrial Science and Technology

<120> Heat-resistant enzyme having β - glycosidase activity

<130> PH-679US

<150> JP 10-222866

<141> 1998-08-06

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 1269

<212> DNA

<213> Pyrococcus horikoshii

<220>

<221> CDS

<222> (1)...(1269)

<400> 1

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Met Pro Leu Lys Phe Pro Glu Met Phe Leu Phe Gly Thr Ala Thr Ser

1

5

10

15

tcc cat cag ata gag gga aat aat aga tgg aat gat tgg tgg tac tat 96

663000-36265660

Ser His Gln Ile Glu Gly Asn Asn Arg Trp Asn Asp Trp Trp Tyr Tyr
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gag cag att gga aag ctc ccc tac aga tct ggt aag gct tgc aat cac 144
Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His
35 40 45
tgg gaa ctt tac agg gat gat att cag cta atg acc agc ttg ggc tat 192
Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr
50 55 60
aat gct tat agg ttc tcc ata gag tgg agc agg cta ttc cca gag gaa 240
Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu
65 70 75 80
aat aaa ttt aat gaa gat gct ttc atg aaa tac cgg gag att ata gac 288
Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp
85 90 95
ttg tta ttg acg aga ggt ata act ccc ctg gtg acc cta cac cac ttt 336
Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe
100 105 110
act agc cct ctc tgg ttc atg aag aaa ggt ggc ttc ctt agg gag gag 384
Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu
115 120 125
aac cta aaa cat tgg gaa aag tac ata gaa aag gtt gct gag ctt tta 432
Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu
130 135 140
gaa aaa gtt aaa cta gta gct acc ttc aat gag ccg atg gta tac gta 480
Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val
145 150 155 160
atg atg gga tat cta acg gct tat tgg ccc cca ttc att agg agt cca 528
Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro
165 170 175

66300" 326366

ttt aag gcc ttt aag gta gct gca aac ctg ctt aaa gct cac gca att 576
Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile
180 185 190
gcc tat gaa ctt ctt cat ggg aaa ttc aaa gtt gga atc gta aag aat 624
Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn
195 200 205
att ccc ata ata ctc cca gcg agt gac aag gag agg gat aga aaa gcc 672
Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala
210 215 220
gct gag aaa gct gat aat tta ttt aac tgg cac ttt ttg gat gcg ata 720
Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile
225 230 235 240
tgg agt ggg aaa tac aga ggg gta ttt aaa aca tat agg att ccc caa 768
Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln
245 250 255
agt gac gca gat ttc att ggg gtt aac tat tac acg gcc agc gaa gta 816
Ser Asp Ala Asp Phe Ile Gly Val Asn Tyr Tyr Thr Ala Ser Glu Val
260 265 270
agg cat act tgg aat cct tta aaa ttc ttc ttt gag gtg aaa tta gcg 864
Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala
275 280 285
gat att agc gag agg aag act caa atg gga tgg agc gtt tat cca aaa 912
Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys
290 295 300
gga ata tac atg gcc ctt aaa aaa gct tcc agg tat gga agg cct ctt 960
Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Arg Tyr Gly Arg Pro Leu
305 310 315 320
tat att acg gaa aac gga ata gcg acg ctt gat gat gaa tgg aga gtg 1008
Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val

Ser His Gln Ile Glu Gly Asn Asn Arg Trp Asn Asp Trp Trp Tyr Tyr
 20 25 30
 Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His
 35 40 45
 Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr
 50 55 60
 Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu
 65 70 75 80
 Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp
 85 90 95
 Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe
 100 105 110
 Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu
 115 120 125
 Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu
 130 135 140
 Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val
 145 150 155 160
 Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro
 165 170 175
 Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile
 180 185 190
 Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn
 195 200 205
 Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala
 210 215 220
 Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile
 225 230 235 240
 Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln

245	250	255	
Ser Asp Ala Asp Phe Ile	Gly Val Asn Tyr Tyr Thr Ala Ser Glu Val		
260	265	270	
Arg His Thr Trp Asn Pro	Leu Lys Phe Phe Phe Glu Val Lys Leu Ala		
275	280	285	
Asp Ile Ser Glu Arg Lys Thr	Gln Met Gly Trp Ser Val Tyr Pro Lys		
290	295	300	
Gly Ile Tyr Met Ala Leu Lys	Lys Ala Ser Arg Tyr Gly Arg Pro Leu		
305	310	315	320
Tyr Ile Thr Glu Asn Gly Ile	Ala Thr Leu Asp Asp Glu Trp Arg Val		
325	330	335	
Glu Phe Ile Ile Gln His Leu	Gln Tyr Val His Lys Ala Ile Glu Asp		
340	345	350	
Gly Leu Asp Val Arg Gly Tyr Phe	Tyr Trp Ser Phe Met Asp Asn Tyr		
355	360	365	
Glu Trp Lys Glu Gly Phe Gly Pro	Arg Phe Gly Leu Val Glu Val Asp		
370	375	380	
Tyr Gln Thr Phe Glu Arg Arg Pro	Arg Lys Ser Ala Tyr Val Tyr Gly		
385	390	395	400
Glu Ile Ala Arg Ser Lys Glu Ile	Lys Asp Glu Leu Leu Lys Arg Tyr		
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420			

<210> 3

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: An upper primer designed to create the NdeI site.

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<210> 4

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: A lower primer designed to create the BamHI site.

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